

## SEQUENCE LISTING

&lt;110&gt; The Chemo-Sero-Therapeutic Research Institute

&lt;120&gt; A DNA coding for merozoite protein of Babesia caballi, a recombinant protein obtained by using said DNA and a use thereof

&lt;130&gt; 661440

&lt;160&gt; 2

&lt;210&gt; 1

&lt;211&gt; 1828

&lt;212&gt; DNA

&lt;213&gt; Babesia caballi

&lt;400&gt; 1

GTGCCCTGGC CGTTGCCAC AACAGCCGTG TTTCATC ATG GCT OCC AGC GAC TCT	56
Met Ala Pro Ser Asp Ser	
1 5	
GTG GGC GAC GTG ACT AAG ACC TTA TTG GCT GCC AGC GAA AGT GTG GAC	104
Val Gly Asp Val Thr Lys Thr Leu Leu Ala Ala Ser Glu Ser Val Asp	
10 15 20	
TCA GCT GCC AAT GCC TAT ATG ATC AAC AGT GAC ATG AGC GAT TAC TTG	152
Ser Ala Ala Asn Ala Tyr Met Ile Asn Ser Asp Met Ser Asp Tyr Leu	
25 30 35	
TCG GCT GTG TCT GAC AAC TTC GCC GAG CGC ATT TGC AGT CAG GTC CCT	200
Ser Ala Val Ser Asp Asn Phe Ala Glu Arg Ile Cys Ser Gln Val Pro	
40 45 50	
AAG GGG AGT AAC TGC AGT GCT TCC GTT AGC GCA TAC ATG AGT CGC TGC	248
Lys Gly Ser Asn Cys Ser Ala Ser Val Ser Ala Tyr Met Ser Arg Cys	
55 60 65 70	
GCT AAA CAG GAC TGC CTG ACT CTC CAA AGT CTT AAG TAC CCT CTT GAG	296
Ala Lys Gln Asp Cys Leu Thr Leu Gln Ser Leu Lys Tyr Pro Leu Glu	
75 80 85	
GCT AAG TAC CAA CCG CTG ACC CTT CCT GAC CCC TAC CAG TTG GAG GCC	344
Ala Lys Tyr Gln Pro Leu Thr Leu Pro Asp Pro Tyr Gln Leu Glu Ala	
90 95 100	
GCA TTT ATA CTC TTC AAG GAG AGT GAC GCT AAT CCG GCC AAT AGC ACT	392
Ala Phe Ile Leu Phe Lys Glu Ser Asp Ala Asn Pro Ala Asn Ser Thr	
105 110 115	

GAG	AAG	CGC	TTC	TGG	ATG	CGT	TTC	AGA	AGG	GGC	AAG	AAC	CAC	AGT	TAC	440
Glu	Lys	Arg	Phe	Trp	Met	Arg	Phe	Arg	Arg	Gly	Lys	Asn	His	Ser	Tyr	
120						125					130					
TTC	CAC	GAC	TTA	GTC	TTC	AAT	CTG	CTG	GAG	AAG	AAC	GTG	ACT	CGC	GAC	488
Phe	His	Asp	Leu	Val	Phe	Asn	Leu	Leu	Glu	Lys	Asn	Val	Thr	Arg	Asp	
135					140					145				150		
CGC	GAT	GCT	ACT	GAC	ATT	GAG	AAC	TTT	GGC	TCC	AGG	TAC	CTG	TAC	ATG	536
Ala	Asp	Ala	Thr	Asp	Ile	Glu	Asn	Phe	Ala	Ser	Arg	Tyr	Leu	Tyr	Met	
				155				160					165			
GCC	ACG	CTT	TAC	TAC	AAG	ACG	TAC	ACG	AAT	GTT	GAT	GAG	TTC	GGT	GCT	584
Ala	Thr	Leu	Tyr	Tyr	Lys	Thr	Tyr	Thr	Asn	Val	Asp	Glu	Phe	Gly	Ala	
				170				175					180			
AGC	TTC	TTT	AAC	AAG	TTG	TCT	TTC	ACT	ACT	GGG	TTG	TTC	GGC	TGG	GGC	632
Ser	Phe	Phe	Asn	Lys	Leu	Ser	Phe	Thr	Thr	Gly	Leu	Phe	Gly	Trp	Gly	
	185					190				195						
ATC	AAG	AGG	GCA	CTT	AAG	CAG	ATT	ATT	CGC	TCT	AAC	CTG	CCC	CTT	GAC	680
Ile	Lys	Arg	Ala	Leu	Lys	Gln	Ile	Ile	Arg	Ser	Asn	Leu	Pro	Leu	Asp	
200					205					210						
ATC	GGG	ACA	GAA	CAC	AGC	GTC	AGT	CGC	CTG	CAG	CAC	ATT	ACG	AGC	AGT	728
Ile	Gly	Thr	Glu	His	Ser	Val	Ser	Arg	Leu	Gln	His	Ile	Thr	Ser	Ser	
215				220				225				230				
TAC	AAG	GAT	TAC	ATG	GAT	ACG	CAG	ATT	CCT	GCA	CTG	CCC	AAG	TTT	GGC	776
Tyr	Lys	Asp	Tyr	Met	Asp	Thr	Gln	Ile	Pro	Ala	Leu	Pro	Lys	Phe	Ala	
				235				240				245				
AAG	CGT	TTC	TCC	CTT	ATG	GTA	GTG	CAG	AGG	CTG	CTG	GCC	ACC	GTG	GCT	824
Lys	Arg	Phe	Ser	Leu	Met	Val	Val	Gln	Arg	Leu	Leu	Ala	Thr	Val	Ala	
			250					255				260				
GGT	TAC	GTC	GAC	ACC	CCG	TGG	TAT	AAG	AAG	TGG	TAC	ATG	AAG	CTG	AAG	872
Gly	Tyr	Val	Asp	Thr	Pro	Trp	Tyr	Lys	Lys	Trp	Tyr	Met	Lys	Leu	Lys	
			265					270				275				
AAC	TTT	ATG	GTG	AAC	AGG	GTG	TTC	ATT	CCT	ACA	AAG	AAG	TTC	TTC	AAT	920
Asn	Phe	Met	Val	Asn	Arg	Val	Phe	Ile	Pro	Thr	Lys	Lys	Phe	Phe	Asn	
			280					285				290				
AAG	GAA	ATT	CGT	GAG	CCT	AGT	AAG	GCA	TTA	AAA	GAA	AAG	GTG	TCA	ACC	968
Lys	Glu	Ile	Arg	Glu	Pro	Ser	Ser	Lys	Ala	Leu	Lys	Glu	Lys	Val	Ser	Thr
295				300						305				310		

GAC ACC AAG GAT TTA TTC GAG AAC AAA ATT GGG CAG GGT ACT GTG GAC	1016
Asp Thr Lys Asp Leu Phe Glu Asn Lys Ile Gly Gln Gly Thr Val Asp	
315 320 325	
TTC TTC AAT AAG GAA ATT CGT GAC CCT AGT AAG GCA TTA AAA GAA AAA	1064
Phe Phe Asn Lys Glu Ile Arg Asp Pro Ser Lys Ala Leu Lys Glu Lys	
330 335 340	
GTG TCA AAC GAC GCC AAG GAT TTA TTC GAG AAC AAA ATT GGG CAG GGT	1112
Val Ser Asn Asp Ala Lys Asp Leu Phe Glu Asn Lys Ile Gly Gln Gly	
345 350 355	
ACT GTG GAC TTC ATC AAT AAC GAA ATT CGT GAC CCT AGT AAG GCA TTA	1160
Thr Val Asp Phe Ile Asn Asn Glu Ile Arg Asp Pro Ser Lys Ala Leu	
360 365 370	
ATA AGA AAA GTG TCA ACG GGG GCC GAG GAT TTA TTC GAG AAC AAA ATT	1208
Ile Arg Lys Val Ser Thr Gly Ala Glu Asp Leu Phe Glu Asn Lys Ile	
375 380 385 390	
GGG CAG GGT ACT GTG GAC TTC ATC AAT AAC GAA ATT CGT GAC CCT AGT	1256
Gly Gln Gly Thr Val Asp Phe Ile Asn Asn Glu Ile Arg Asp Pro Ser	
395 400 405	
AAG GCA TTA ATA AGA AAA GTG TAC ACC GAG GCC GAT GAT TTA TTC GAG	1304
Lys Ala Leu Ile Arg Lys Val Tyr Thr Glu Ala Asp Asp Leu Phe Glu	
410 415 420	
AAC AAA ATT GGG CAG GGT ACT GTG GAC TTC ATC AAT AAG GAA ATT CGT	1352
Asn Lys Ile Gly Gln Gly Thr Val Asp Phe Ile Asn Lys Glu Ile Arg	
425 430 435	
GAC CCT AGT AAG GCA TTA ATA AGA AAA GTG TCT ACC GAG GCC GAT AAT	1400
Asp Pro Ser Lys Ala Leu Ile Arg Lys Val Ser Thr Glu Ala Asp Asn	
440 445 450	
TTA TTG GAG AAA TAGGTTGCGA AGCCCTGAG GAAGCACC GC AAGGGCAACG TTAGT	1457
Leu Leu Glu Lys	
455	
GACAGCGGG AATCTGAGGA AATTTCGGCT GTGGTGAAT CTTTGAATC CGACAACGAA	1517
ATGAAGACCC AGGAGTCAAT GAACTCGGAG AGTGCTTCTA CCGAACTCCC TTCTGAGGAG	1577
TCCGAGGAAG AGTCGGCTGC TATGTTATT CAGCAGCCCA CCTTGAGGA GGCAGCCAG	1637
ATCGATTGC CTGCTGAAGA AGACAGCTCA GAGTTGCAGG AAACCTCCGA CAACTATGAA	1697
GCCTCTCTCT AGTCACCTTT GACGTCCATC GCACTGCTCG GAGAATATAA AACGATTGCG	1757
TCGGTTGCAC TCTAGTTGTT AACAATGCAC AATTTAATGT TATAGTTGTT TTGAAAAAAA	1817